AMENDMENTS TO THE CLAIMS

This Listing of Claims will replace all prior versions and Listings of Claims in the application:

Listing of Claims:

Claims 1-22 (cancelled)

Claim 23 (currently amended): A method ~~for the identification, isolation, or separation of identical nucleic acid fragments~~ comprising:

(a) ~~separately~~ digesting separately [[the]] nucleic acids from a mixture of at least two nucleic acid populations ~~of said populations~~ with at least one restriction enzyme;

(b) ligating an adaptor sequence to the restriction fragments resulting from the digestion in step (a);

(c) amplifying [[the]] adaptor-ligated restriction fragments generated ~~in step (a) and~~ in step (b) using an adaptor-specific primer to produce amplification products having different ends in respect to each of the at least two nucleic acid populations;

(d) hybridizing the amplification products of step (c) from the different nucleic acid populations with each other to generate a mixture comprising homoduplexes and heteroduplexes; [[and]]

(e) eliminating blunt ended homoduplexes from heteroduplexes having forked ends by digesting the homoduplexes with an enzyme that specifically digests blunt-ended double-stranded DNA fragments;

(f) eliminating mismatched heteroduplexes by using mismatch repair enzymes; and

(g) identifying, isolating or separating [[the]] fully-matched ~~heterohybrid fragments~~ heteroduplexes, thereby identifying, isolating or separating nucleic acid fragments that are identical between the at least two nucleic acid populations.

Claim 24 (previously presented): The method of claim 23, wherein said nucleic acid populations comprise genomic DNA populations.

Claim 25(previously presented): The method of claim 24, wherein said nucleic acid populations comprise human genomic DNA populations.

Claim 26 (previously presented): The method of claim 25, wherein said nucleic acid populations comprise nucleic acid populations from different subjects having a common trait of interest.

Claim 27 (previously presented): The method of claim 23, wherein said nucleic acid populations comprise one or more selected chromosomes.

Claim 28 (previously presented): The method of claim 23, wherein said nucleic acid populations comprise nucleic acid populations from different sources.

Claim 29 (previously presented): The method of claim 23, wherein said restriction fragments are size-selected prior to said amplifying step.

Claim 30 (currently amended): The method of claim 23, wherein part or all of said restriction fragments are cloned prior to the amplifying step into a vector in a chromosome-specific and sequence-specific fashion.

Claim 31 (cancelled)

Claim 32 (currently amended): The method of claim [[31]] 23, wherein said adaptor sequence comprises a 5 base to 100 base long double-stranded DNA fragment.

Claim 33 (cancelled)

Claim 34 (previously presented): The method of claim 23, wherein said amplifying step further comprises using a polymerase chain reaction technique.

Claim 35 (cancelled)

Claim 36 (currently amended): The method of claim 23, wherein said primer is labelled by a technique [[chosen]] selected from the group consisting of (a) adding a unique 5'-sequence to the primer; (b) adding a chemical activity to the primer which provides a means to distinguish between or among the amplification products from different said nucleic acid populations; and (c) adding modified nucleotides into the primer, allowing one to distinguish between or among the amplification products from [[different said]] the nucleic acids of the at least two populations.

Claim 37 (cancelled)

Claim 38 (cancelled)

Claim 39 (currently amended): The method of claim [[38]] 23, wherein said eliminating step (f) comprises incubating the hybridization mixture of step (d) with MutS, MutL, and MutH, resulting in a specific cleavage of mismatched heteroduplexes [[hybrids]].

Claim 40 (cancelled)

Claim 41 (cancelled)

Claim 42 (cancelled)

Claim 43 (cancelled)

Claim 44 (cancelled)

Claim 45 (cancelled)

Claim 46 (withdrawn): A kit suitable for genetic analysis according to the method of claim 23, comprising:

(a) a double stranded adaptor molecule; and

(b) a specific, labeled primer.

Claim 47 (withdrawn): The kit of claim 46, further comprising control deoxyribonucleic acids.

Claim 48 (withdrawn): The kit of claim 46, further comprising a means for the detection of selected DNA fragments.

Claim 49 (withdrawn): The kit of claim 46, further comprising a means for the detection of selected DNA fragments.

Claim 50 (withdrawn): The kit of claim 49, wherein said means comprises an ordered DNA array.

Claim 51 (withdrawn): The kit of claim 49, wherein said means comprises coded beads carrying specific DNA sequences.

Claim 52 (withdrawn): A method of separating identical DNA fragments from complex mixtures of at least two nucleic acid populations, comprising:

(a) hybridizing the populations; and

(b) separating the fully-matched heterohybrids formed via the hybridization;

wherein said nucleic acid populations comprise amplified nucleic acids.

Claim 53 (withdrawn): A method of identifying DNA regions that are relevant to a pathological condition or a particular trait, comprising:

(a) hybridizing at least two nucleic acid populations from different sources having the particular trait or pathology; and

(b) separating the fully-matched heterohybrids formed which contain DNA regions that are relevant to said pathological condition or particular trait;

wherein said nucleic acid populations are chosen from the group consisting of amplified nucleic acids and pre-selected nucleic acids.

Claim 54 (new): The method of claim 23, wherein the enzyme that specifically digests blunt-ended double-stranded DNA fragments is exonuclease III.

Claim 55 (new): The method of claim 23, wherein the method further comprises after step (e) eliminating newly created single strands.

Claim 56 (new): The method of claim 55, wherein said eliminating newly created single strands comprises binding said newly created single strands to a single strand-specific matrix.